



Fragment
Size
(pdb)

23130
9416
6557
4361
2322
2027
564

A
B
C

1000 →

FIG. 1



FIG. 2A

HsKin-mmKin pep 16 10 1997 16 00										
hsKin17 . pep	10	20	30	40	50	60	70	80	90	100
	MGKSDFLTPK AIANRIKSG LQKLRWYQCM CQKQCRDENG FKCHCMSESH QRQLLASEN PQQFMDYFSE EFRNDFLELL RRRFGTKRVH NNIVYNEYIS									
	*									
mmKin17 . pep	110	120	130	140	150	160	170	180	190	200
	MGKSDFLSPK AIANRIKSG LQKLRWYQCM CQKQCRDENG FKCHCMSESH QRQLLASEN PQQFMDYFSE EFRNDFLELL RRRFGTKRVH NNIVYNEYIS									
hsKin17 . pep	210	220	230	240	250	260	270	280	290	300
	HREHIHMNAT QWETLTDFTK WLGREGLCKV DETPKGWYIQ YIDRDPETIR RQLELEKSKK QQLDDEEKTA KFIEEQVRRG LEGKEQEPT FTELSRENDE									
	* * *									
mmKin17 . pep	310	320	330	340	350	360	370	380	390	400
	HREHIHMNAT QWETLTDFTK WLGREGLCKV DETPKGWYIQ YIDRDPETIR RQLELEKSKK QQLDDEEKTA KFIEEQVRRG LEGKEQEPT FTELSRENDE									
hsKin17 . pep	410	420	430	440	450	460	470	480	490	500
	EKVTFNLKSG ACCSSGATSS KSSSLGPSAL KLLGSAASGK RKESSQSS AQPAKKKKSA LDEIMELEEE KKRTARTDAW LQPGIVVKII TKKLGEKYHK									
	* * * * *									
mmKin17 . pep	510	520	530	540	550	560	570	580	590	600
	EKVTFNLKSG AGGSAGATSS KSSSLGPSAL KLLGSAASGK RKESSQSS AQPAKKKKSA LDEIMELEEE KKRTARTDAW LQPGIVVKII TKKLGEKYHK									
hsKin17 . pep	610	620	630	640	650	660	670	680	690	700
	KKAIWKEVID KYTAVVKMID SGDRLKLDQT HLETVIPAG KRVLVNGGY RGNEGTLES NEKAFSATIV IETGPLKRR VEGIQYEDIS KLA									
	* * *									
mmKin17 . pep	710	720	730	740	750	760	770	780	790	800
	KKGVWKEVID RYTAVVKMTD SGDRLKLDQT HLETVIPAG KRVLVNGGY RGNEGTLES NEKAFSATIV IETGPLKRR VEGIQYEDIS KLA									
hsKin17 . pep	810	820	830	840	850	860	870	880	890	900
	KKGVWKEVID RYTAVVKMTD SGDRLKLDQT HLETVIPAG KRVLVNGGY RGNEGTLES NEKAFSATIV IETGPLKRR VEGIQYEDIS KLA									
mmKin17 . pep	910	920	930	940	950	960	970	980	990	1000
	KKGVWKEVID RYTAVVKMTD SGDRLKLDQT HLETVIPAG KRVLVNGGY RGNEGTLES NEKAFSATIV IETGPLKRR VEGIQYEDIS KLA									

<= =
<= =



FIG. 2B

hsKin17-mmKin17	16	10	1997	15	59						
hsKin17 . seq		10	20	30	40	50	60	70	80	90	100
		TGATTCGAGC	TCGGTACCG	GGGATCCGAT	TAGAAAGTGA	TCGCTGCCGT	GGTCGCCATG	GGGAAGTCGG	ATTTTCTTAC	TCCCAAGGCT	ATCGCCAACA
							*	*	*	*	*
mmKin17 . seq							ATG	GGCAAGTCGG	ATTTTCTGAG	CCCCAAGGCT	ATCGCCAATA
hsKin17 . seq		110	120	130	140	150	160	170	180	190	200
		GGATCAAGTC	CAGAGGGCTG	CAGAAGCTAC	GCTGGTATTG	CCAGATGTGC	CAGAAGCAGT	GCCGGGACGA	GAATGGCTTT	AAGTGTCAAT	GTATGTCGGA
		*	*	*	*	*	*	*	*	*	*
mmKin17 . seq		GAATTAAGTC	CAAAAGGGCTC	CAGAAGCTTC	GCTGGTACTG	CCAGATGTGC	CAAAAGCAAT	GCCGGCAGCA	GAATGGCTTT	AAGTGTCACT	GTATGTCGGA
		210	220	230	240	250	260	270	280	290	300
hsKin17 . seq		ATCTCATCAG	AGACAACATAT	TGCTGGCTTC	AGAAAATCCT	CAGCAGTTTA	TGGATTATT	TTCAGAGGAA	TTCGGAATG	ACTTTCTAGA	ACTTCTCAGG
		*	*	*	*	*	*	*	*	*	*
mmKin17 . seq		ATCTCATCAA	AGACAACCTGT	TGCTGGCTTC	AGAAAACCCCT	CAGCAGTTTA	TGGATTATT	TTCAGAGGAA	TTCGGAATG	ACTTTCTGGA	ACTTCTGAGG
		310	320	330	340	350	360	370	380	390	400
hsKin17 . seq		AGACGCTTTG	GCACATAAAG	GGTCCACAAAC	AACATTGTCT	ACAACGAATA	CATCAGCCAC	CGAGAGGCACA	TCCACATGAA	TGCCACTCAG	TGGGAAACTC
		*	*	*	*	*	*	*	*	*	*
mmKin17 . seq		CGACGCTTTG	GCACATAAAG	GGTCCACAAAC	AACATTGTCT	ACAATGAATA	CATCAGCCAC	CGAGAGGCACA	TCCACATGAA	CGCTACCCAG	TGGGAGACAC
		410	420	430	440	450	460	470	480	490	500
hsKin17 . seq		TGACTGATT	TACTAAGTGG	CTGGGCAGAG	AAGGCTTGIG	CAAAAGTGGAC	GAGACACCAA	AAGGCTGGTA	TATTCAGTAC	ATAGACAGGG	ACCCAGAAAC
		*	*	*	*	*	*	*	*	*	*
mmKin17 . seq		TGACCGACTT	TACCAAGTGG	CTGGGCAGAG	AGGGCTTGIG	TAAAGTGGAT	GAGACACCCA	AAGGCTGGTA	CATTACAGTAC	ATAGACAGAG	ACCCAGAAAC



FIG. 2C

	510	520	530	540	550	560	570	580	590	600
hsKin17 . seq	TATCCGCCGG *	CAACTGGAAC *	TGGAGAAAA **	GAAAAAGCAG *	GACCTTGATG **	ATGAAGAAAA *	AACTGCCAAA *	TTTATTGAAG *	AGCAAGTGAG *	AAGAGGCCCTG
mmKin17 . seq	CATCCGTCGG	CAACTGGAAT	TAGAAAAAA	GAAGAAGCAA	GATCTGGACG	ATGAAGAAAA	AACTGCCAAG	TTCATTGAGG	AGCAGGTGAG	AAGAGGCCCTG
	610	620	630	640	650	660	670	680	690	700
hsKin17 . seq	GAAGGGAAGG	AACAGGAGGT	CCCTACTTTT	ACGGAATTAA	GCAGAGAAAA	TGATGAAGAG	AAAGTCACGT	TTAATTGAG	TAAAGGAGCA	TGTAGCTCAT
mmKin17 . seq	GAAGGGAAGG	AGCAGGAGAC	ACCTGTTTTT	ACAGAACTTA	GCCGAGAAAA	TGAGGAAGAA	AAAGTTACGT	TCAATCTGAA	TAAAGGAGCG	GGTGGCTCAG
	710	720	730	740	750	760	770	780	790	800
hsKin17 . seq	CCGGAGCAAC	ATCTTCCAAG	TCAAGTACTC	TGGGACCCGAG	TGGCACTGAA	ACGATAGGAA	GTTCAGCATC	AGTGAAACGA	AAAGAACTCT	CCCAGAGCTC
mmKin17 . seq	CGGGAGCTAC	AACATCCAAG	TCAAGCTCTT	TGGGACCCAAG	TGGCACTGAAG	CTGCTGGGGA	GCGCAGCATC	CGGGAACCGG	AAAGAGTCTT	CACAGAGCTC



FIG. 2D

hsKin17-mmKin17 16 10 1997 15 59

	810	820	830	840	850	860	870	880	890	900
hsKin17 . seq	AACCTAGTCT *** * *** ***	AAAGAAAAGA * *** ***	AGAAAAGAA * *** ***	ATCTGCATG * *** ***	GATGAAATCA * *** ***	TGGAGATTGA * *** ***	AGAGGAAAG * *** ***	AAAAGAACTG * *** ***	CCCGAAGAGA * *** ***	CTACTGGCTA * *** ***
mmKin17 . seq	CGCCAGCCT GA	GC GA	AGAGAAGAA GTCGGCCCTG	GATGAGATCA GATGAGATCA	TGGAGCTCGA TGGAGCTCGA	AGAGGAAAG AGAGGAAAG	AAAAGGACCG AAAAGGACCG	CACGGACAGA CACGGACAGA	CGCCTGGTTA CGCCTGGTTA	1000
hsKin17 . seq	CAGCCTGAAA * ** * **	TTATTGTGAA * ** * **	AATTATAACC * * **	AGAAACTGG * * **	GAGAGAAATA * * **	TCATAAGAA * * **	AAAGGCTATT * * **	GTTAAGGAAG * * **	TAATTGACAA * * **	ATATACAGCT * * **
mmKin17 . seq	CAGCCGGGGA 1010	TCGTTGTGAA 1020	AATTATAACG 1030	AGGAAGCTTG 1040	GGGAGAAATA 1050	TCACAAGAA 1060	AAAGGGG TC 1070	GTTAAGGAAG 1080	TGATTGACAG 1090	GTACACAGCT 1100
hsKin17 . seq	GTTGTGAAGA * * *	TGATTGATT * * *	TGGAGACAAG * * *	CIGAAACTTG * * *	ACCAGACTCA * * *	TTTAGAGACA * * *	GTAATTCAG * * *	CACCAGGAAA * * *	AAGAATICTA * * *	GTTTAAATG * * *
mmKin17 . seq	GTGGTAAGA 1110	TGACTGACTC 1120	TGGAGACAGG 1130	CTGAAGCTGG 1140	ACCAGACTCA 1150	TTTAGAGACA 1160	GTCAATCCGG 1170	CCCCGGGAA 1180	AAGGGTICTA 1190	GTTTAAATG 1120
hsKin17 . seq	GAGGCTACAG AGGAAATGAA	GGTACCCCTAG * * *	AATCCATCAA * * *	TGAGAGAGCT * * *	TTTTCAGCTA * * *	CTATCGTCAI * * *	TGAAGCTGGC * * *	CCTTTAAAG * * *	GACGCAGAGT * * *	
mmKin17 . seq	GAGGCTACAG AGGAAATGAA	GGCAGCTCTCG * * *	AATCCATCAA * * *	TGAGAGAGCT * * *	TTTTCAGCTA * * *	CGATAGTCAI * * *	TGAAGCTGGA * * *	CCTTTGAAG * * *	GACGCAGAGT * * *	

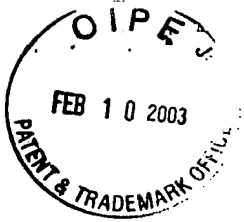


FIG. 2E

	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
hsKin17 . seq	TGAAGGAATT	CAATATGAAG	ACATTCTCTAA	ACTTGCCTGA	GTTTGAAAAT	TGTTAACAA	TACCTTTTAAA	ATCT TAAAG	CATCAAAATTG	GTGTTGCG
	*		*	*		*	**	*	*	*
mmKin17 . seq	TGAAGGTAAT	CAATATGAAG	ACATATCTAA	ACTTGCCTGA	GTTTGAAAAT	TGATAACAA	CACA TTGAA	A CIGTGAAG	CATCAAAATTG	GIGTTAGCCA
	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400
hsKin17 . seq	*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
mmKin17 . seq	AGGCACCTGTG	TAACTCTACT	GTGTTAGGGG	ATTTGTTTTG	TATTAAAAAA	AAAAAAATCA	TCTATTTAAA	TACTAGTGAA	TAGTTGGGTA	AATTATATAAT
	1410	1420	1430	1340	1450		1470	1480	1490	1500
hsKin17 . seq	*****	*****	*****	*****	*****					
mmKin17 . seq	AAAAATCTATG	TTTTTTTTTAA	GTGTAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAA				



FIG. 3A

Kin-17

heart
brain
placenta
lung
liver
skeletal muscle
kidney
pancreas

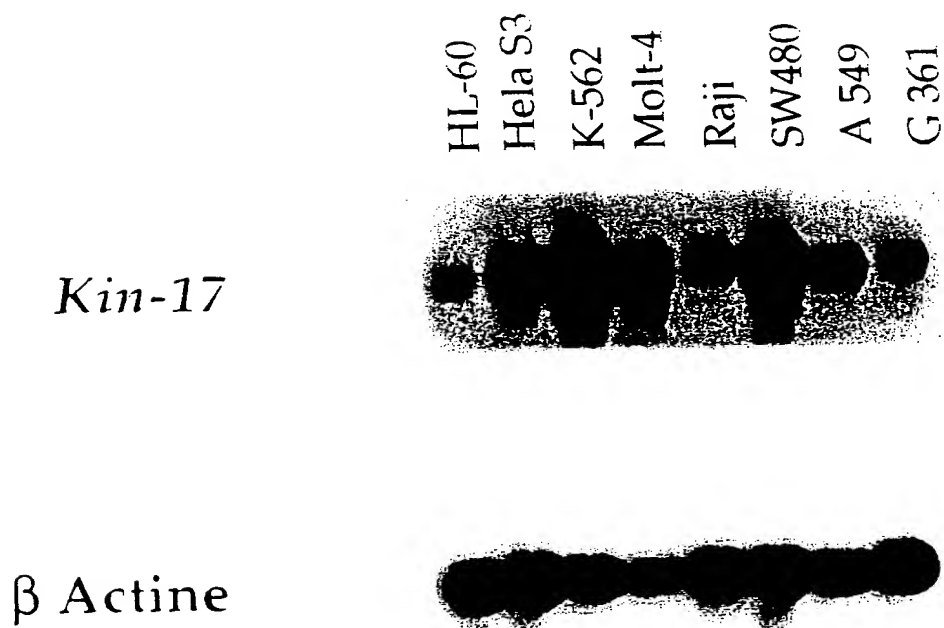
spleen
thymus
prostate
testicle
ovary
small intestine
colon
peripheral blood leukocyte

β Actin





FIG. 3B



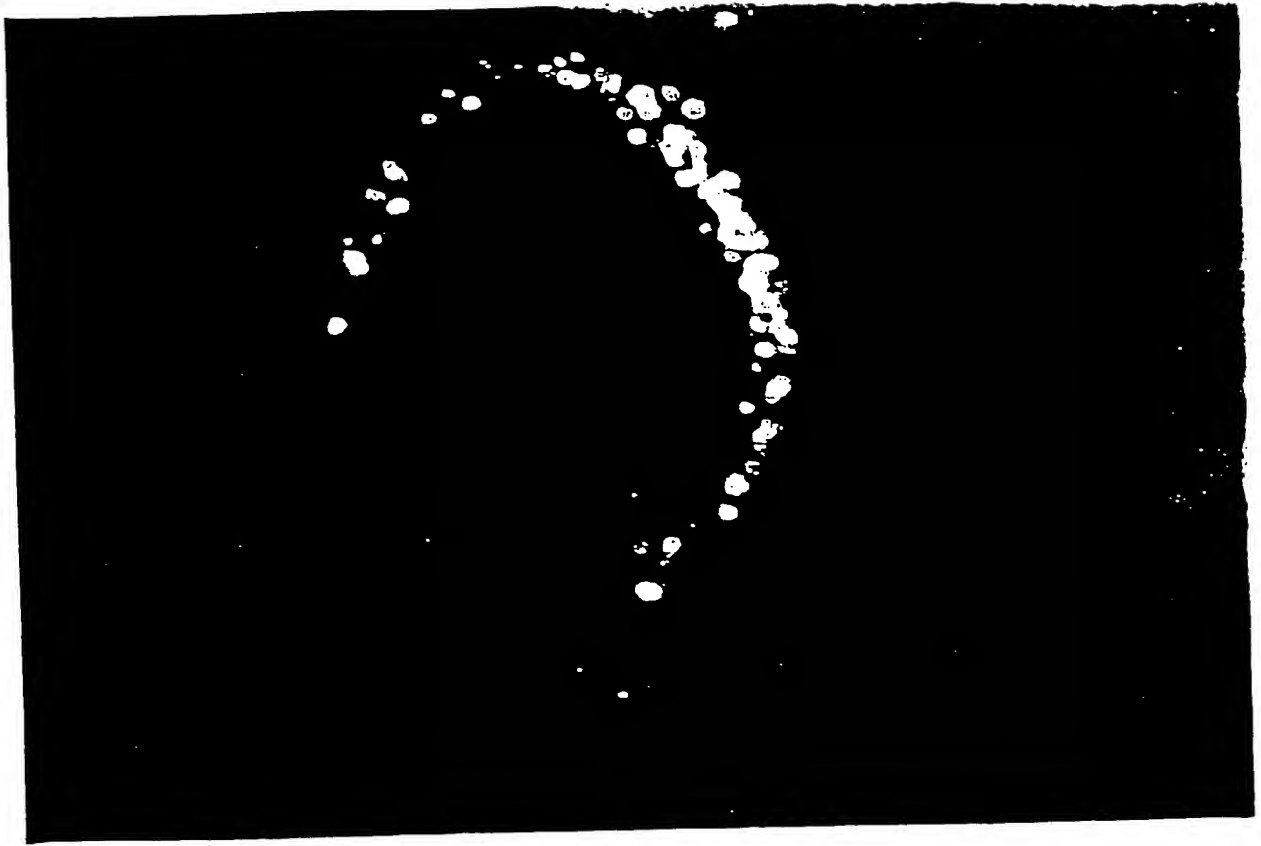


FIG. 4A

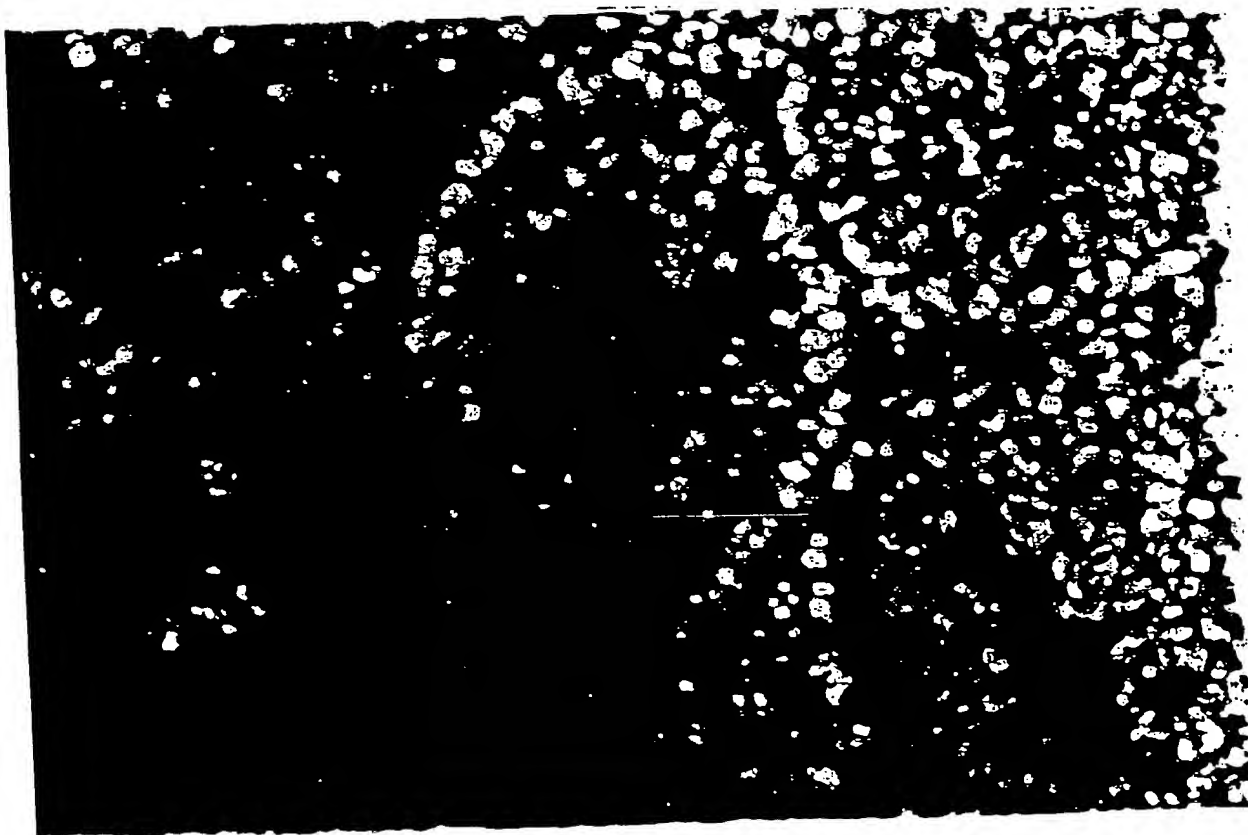
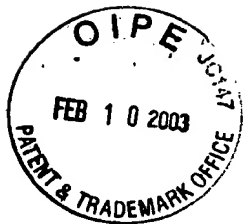


FIG. 4B

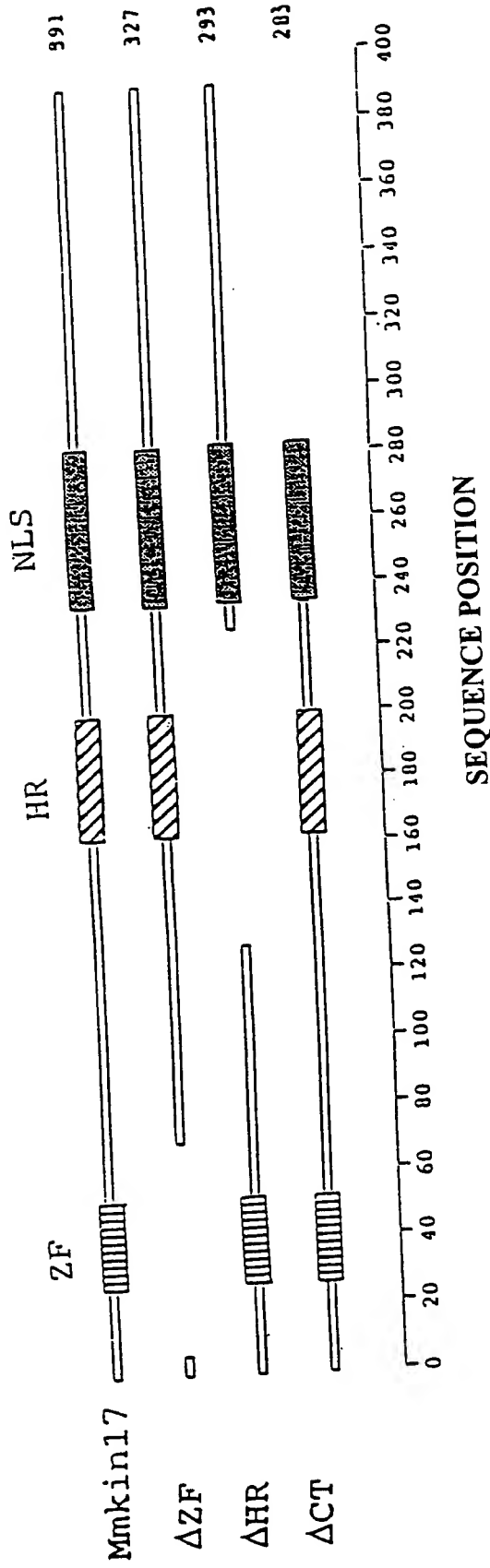


FIG. 5



FIG. 6A

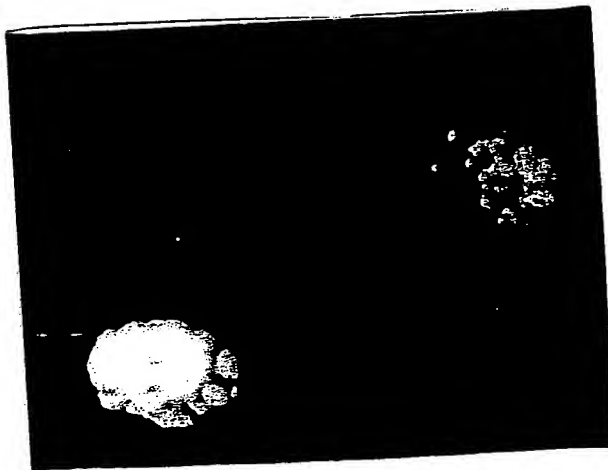


FIG. 6B



Ab2864

FIG. 7B

Ab2864

FIG. 7A

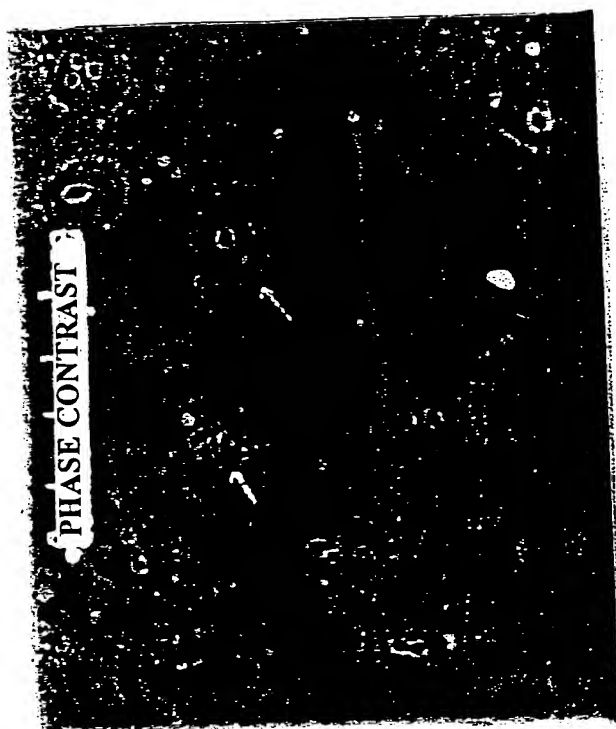
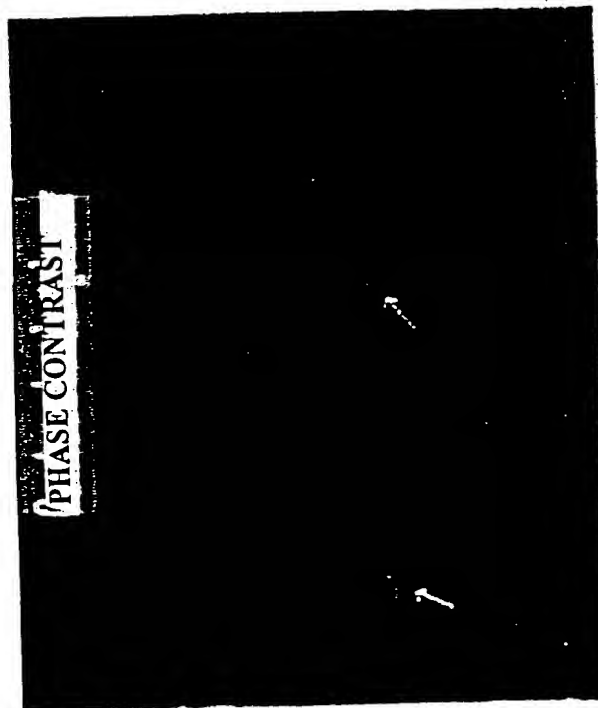
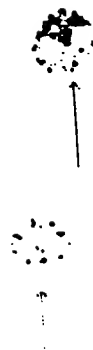




FIG. 8A

DAPI

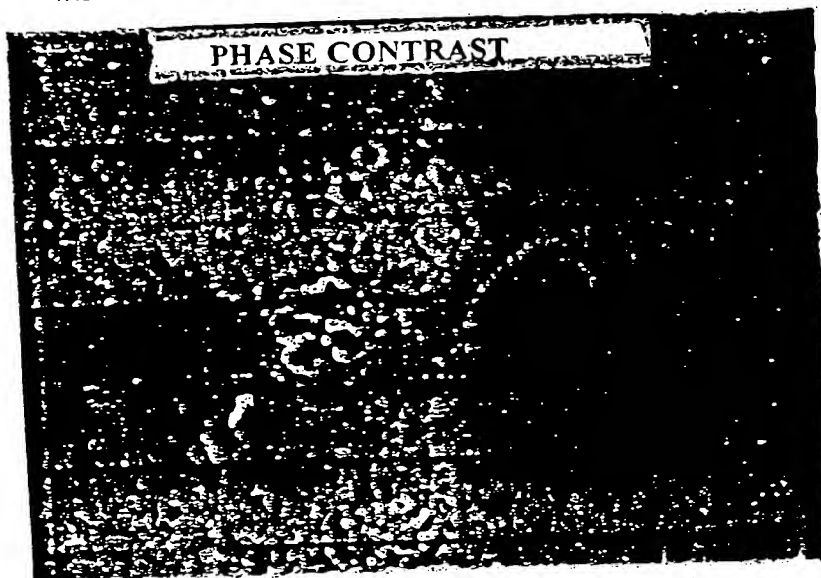
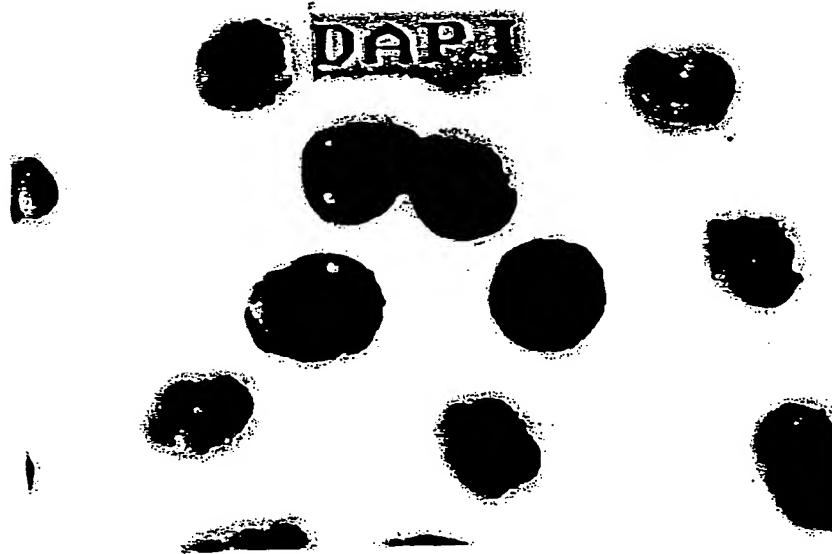
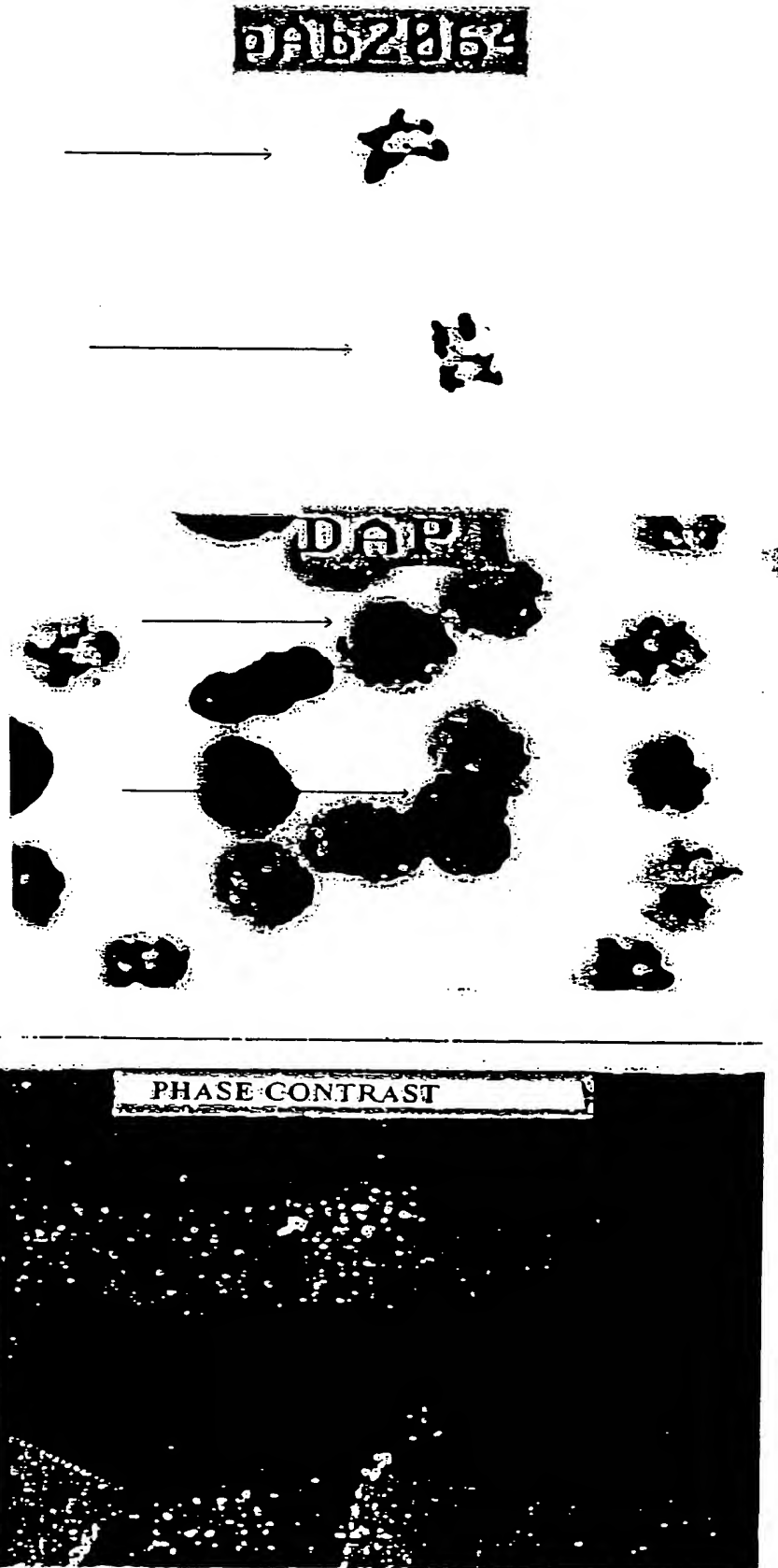




FIG. 8B



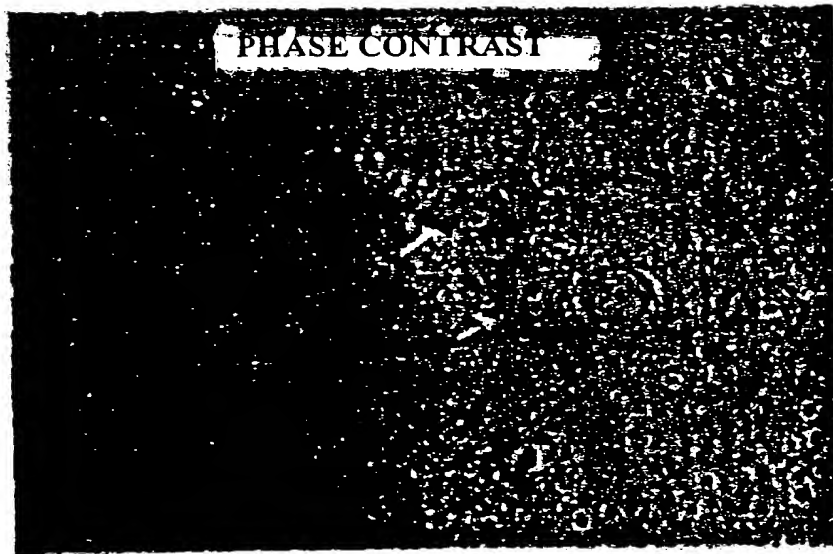
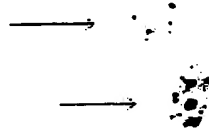


FIG. 9

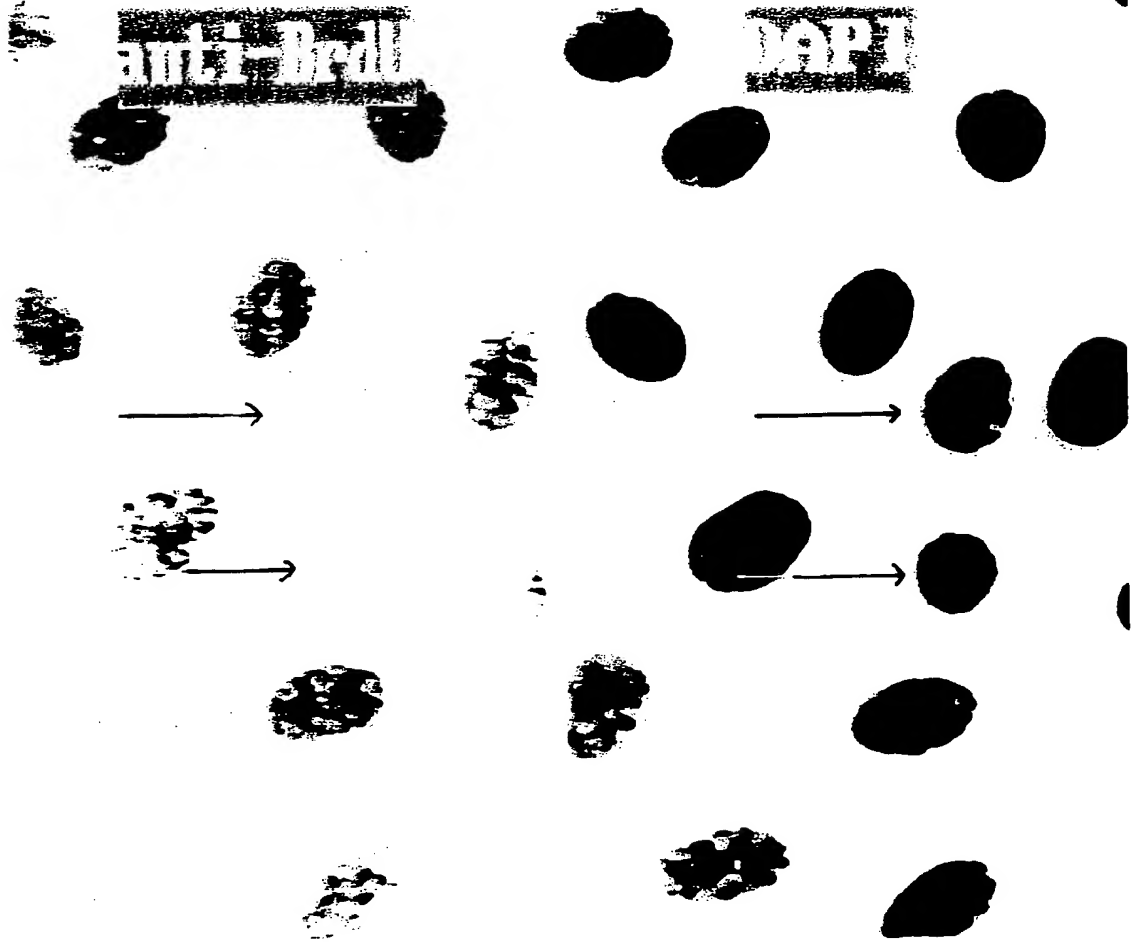
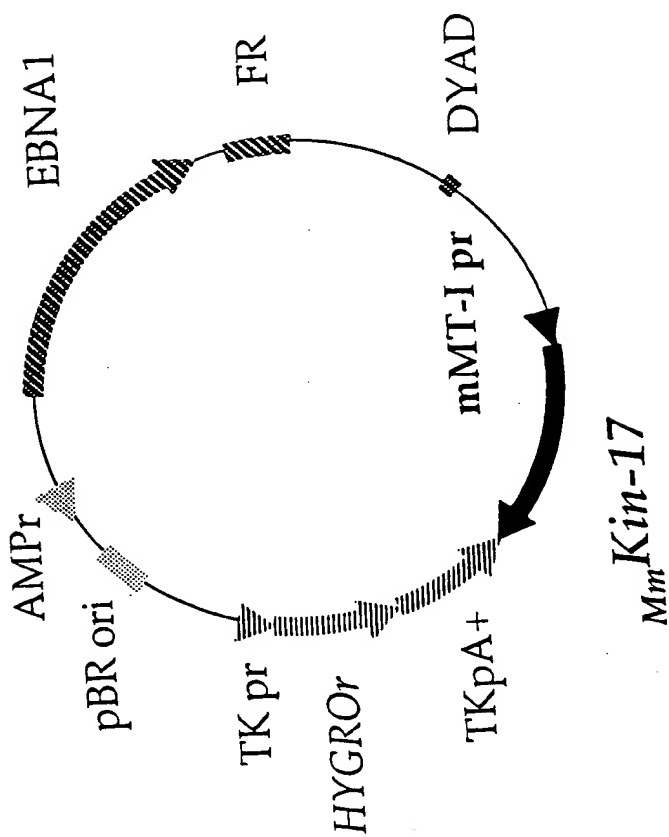


FIG. 10A



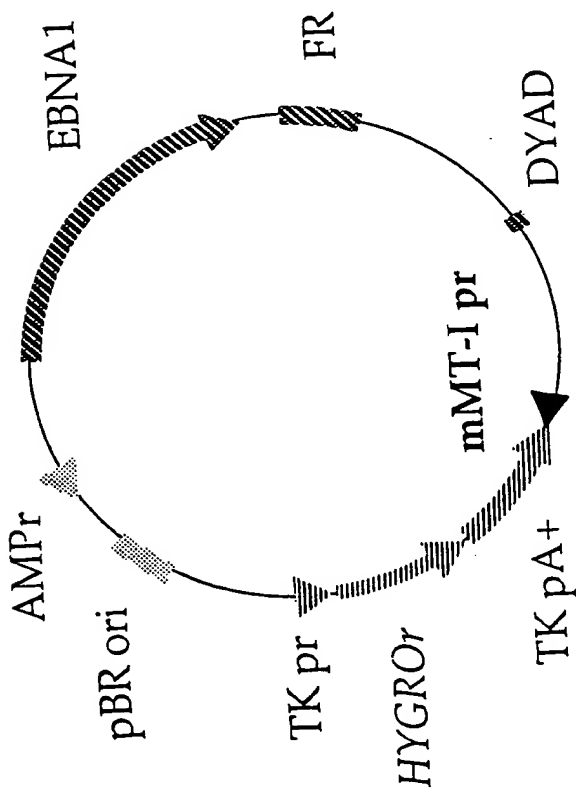
PROTEIN EXPRESSED	NONE	kin17 LOW LEVEL	kin17 HIGH LEVEL	kinΔHR	kinΔCT
% of Cells REPLICATING THEIR DNA	40	40	0	0	33

FIG. 10B



pEBVMT_{Mm}Kin17 (pB223)
(10271 bp)

FIG. 11B



pEBVMTΔ (pB220)
(8824 bp)

FIG. 11A



FIG. 12A

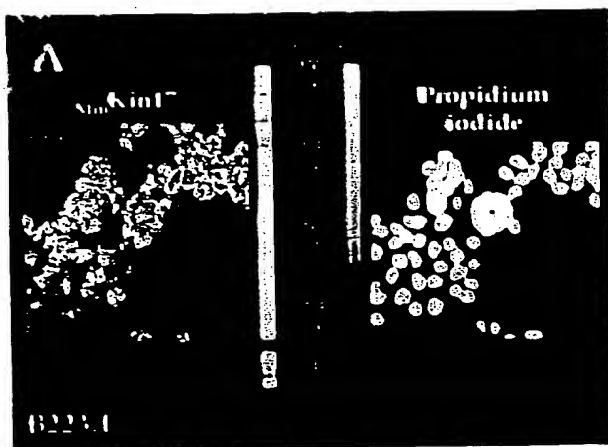


FIG. 12B

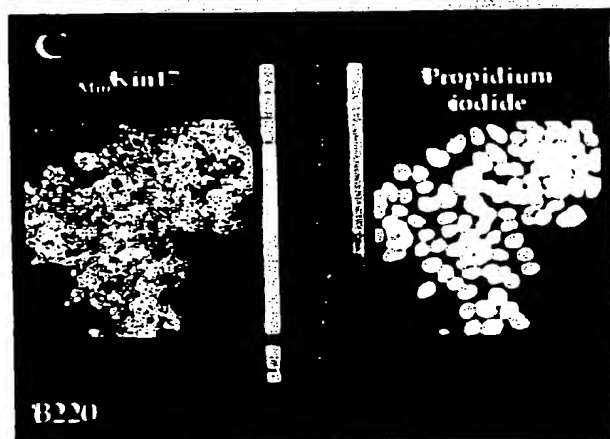
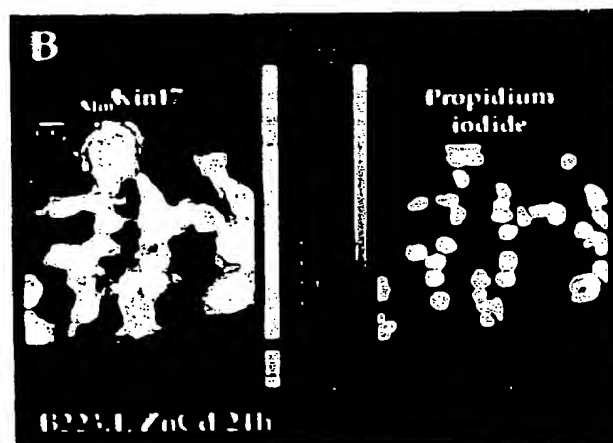


FIG. 12C

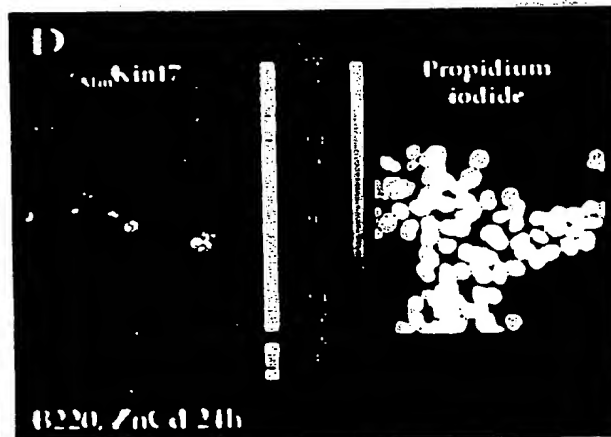


FIG. 12D

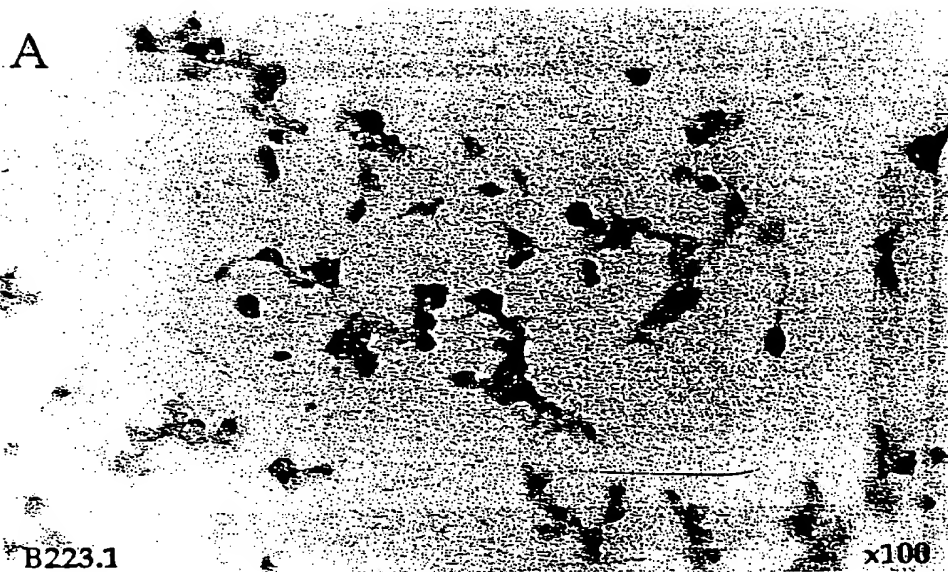


FIG. 13A

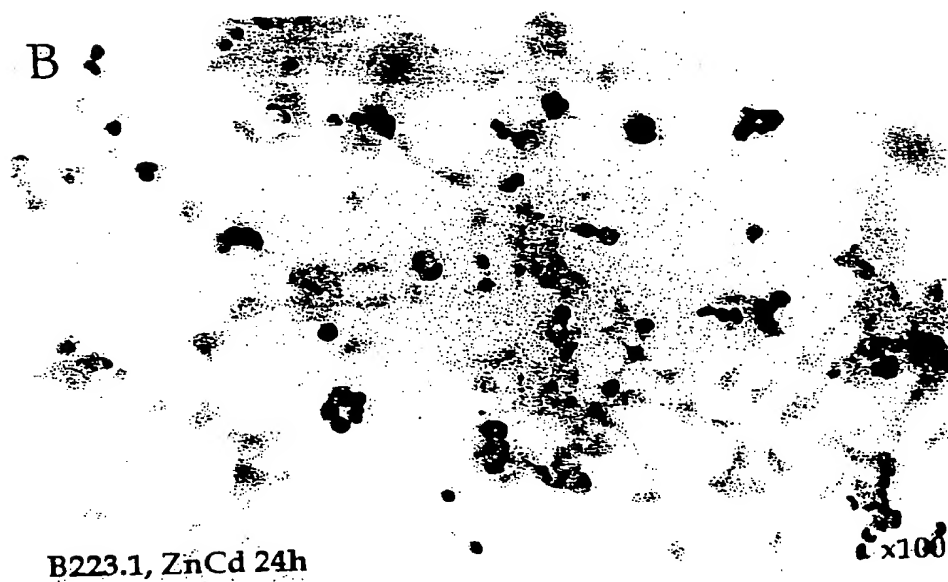


FIG. 13B

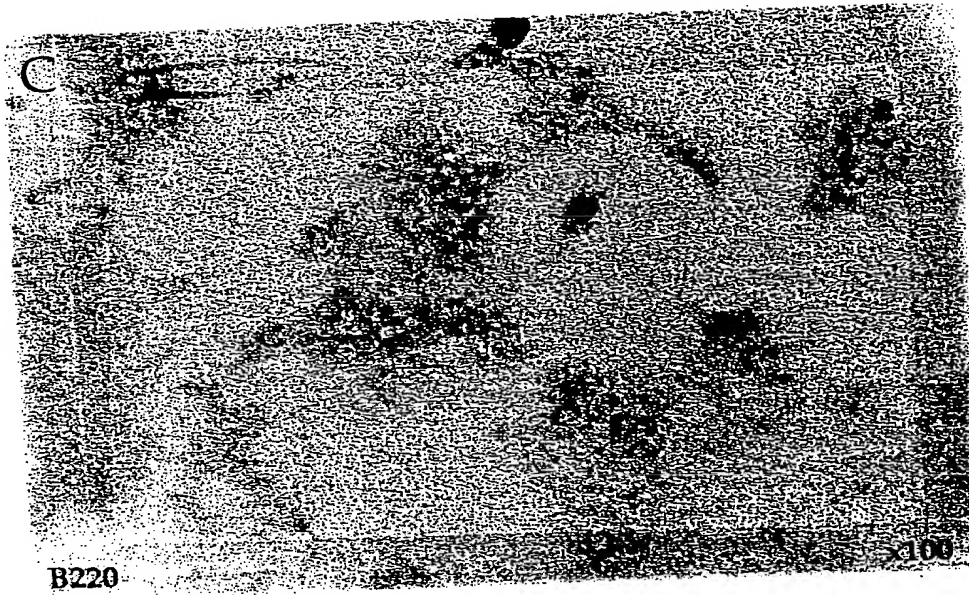


FIG. 13C

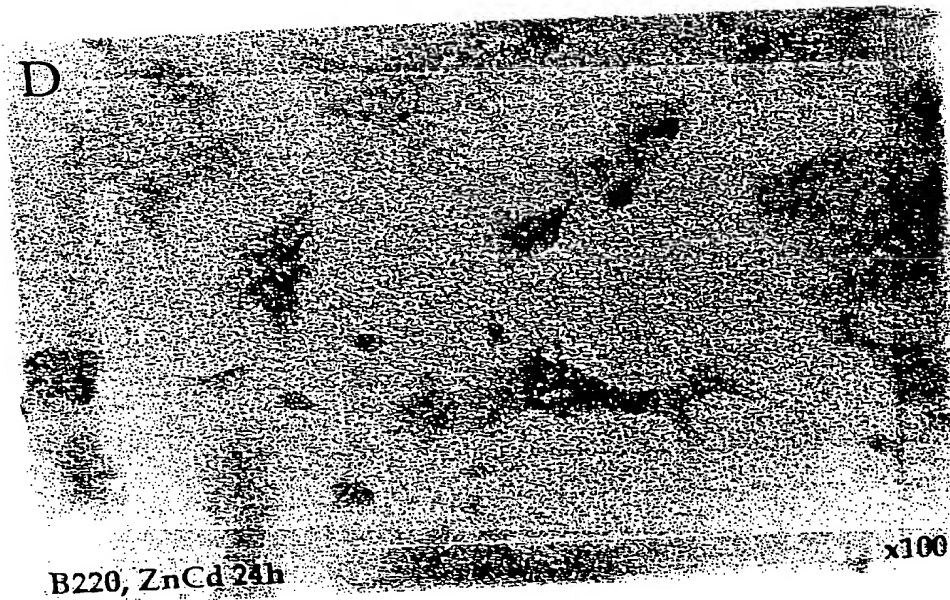


FIG. 13D



FIG. 14B



x1000

x1260

FIG. 14D

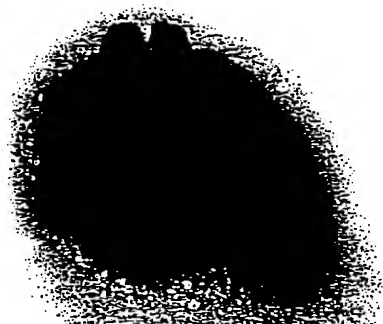


FIG. 14A

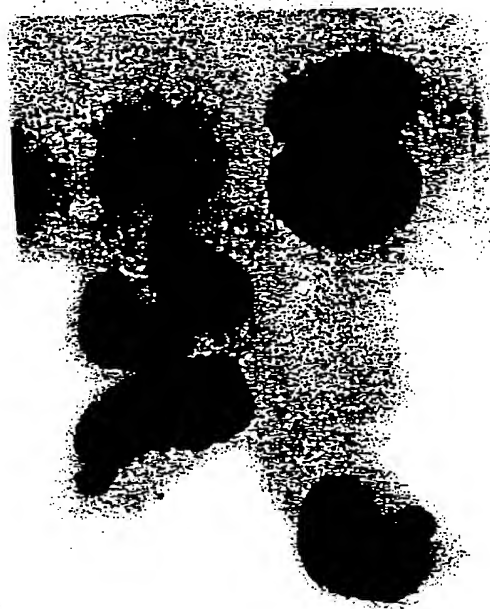


x504

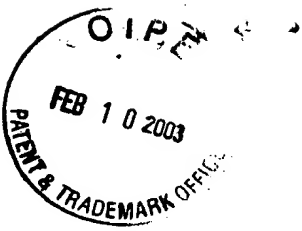
C

x1000

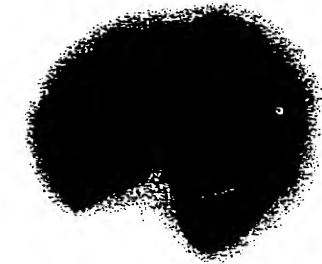
FIG. 14C



D



F



E

x1260

x2000

FIG. 14F

FIG. 14E

OIP
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PATENT & TRADEMARK OFFICE

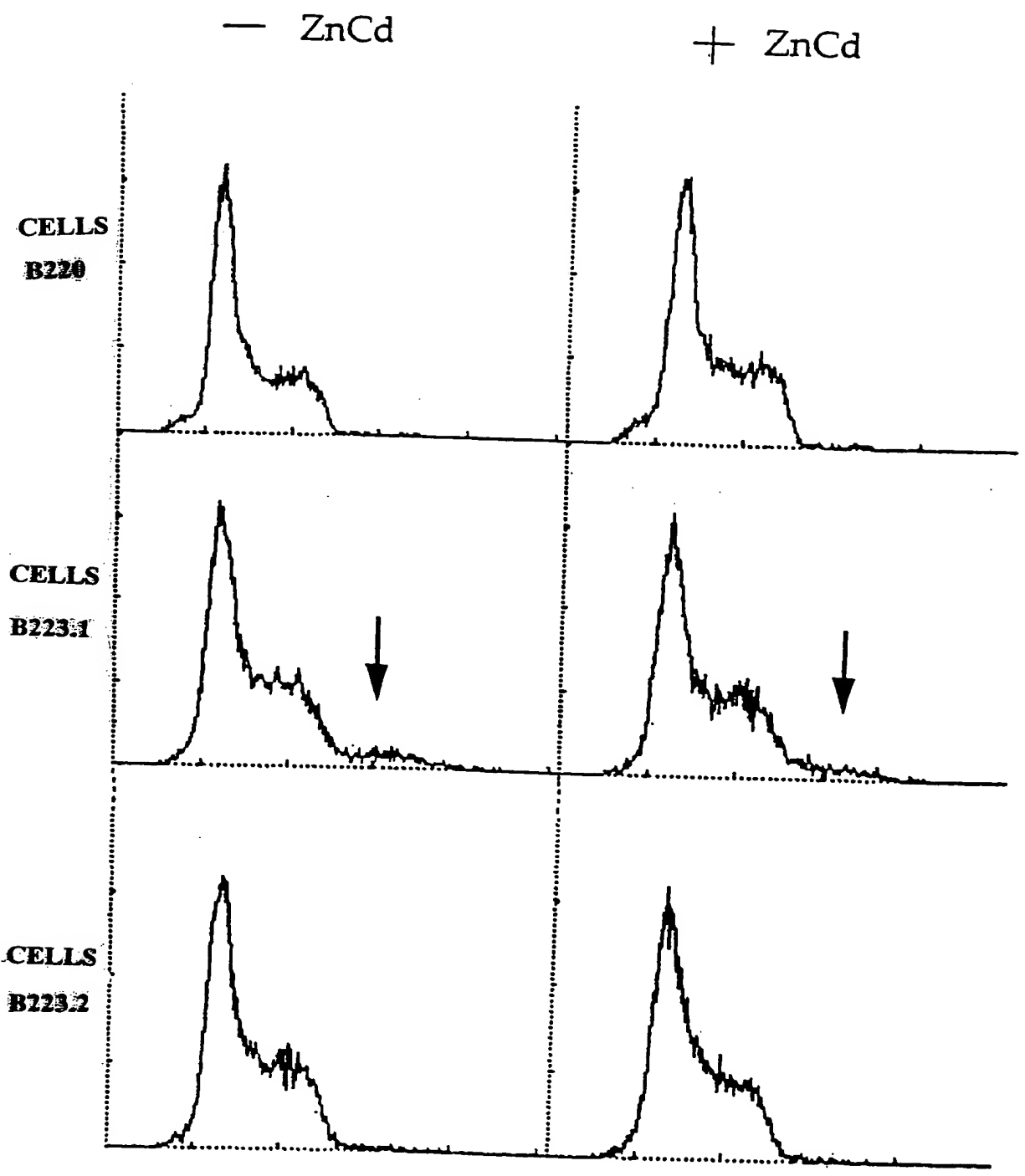


FIG. 15

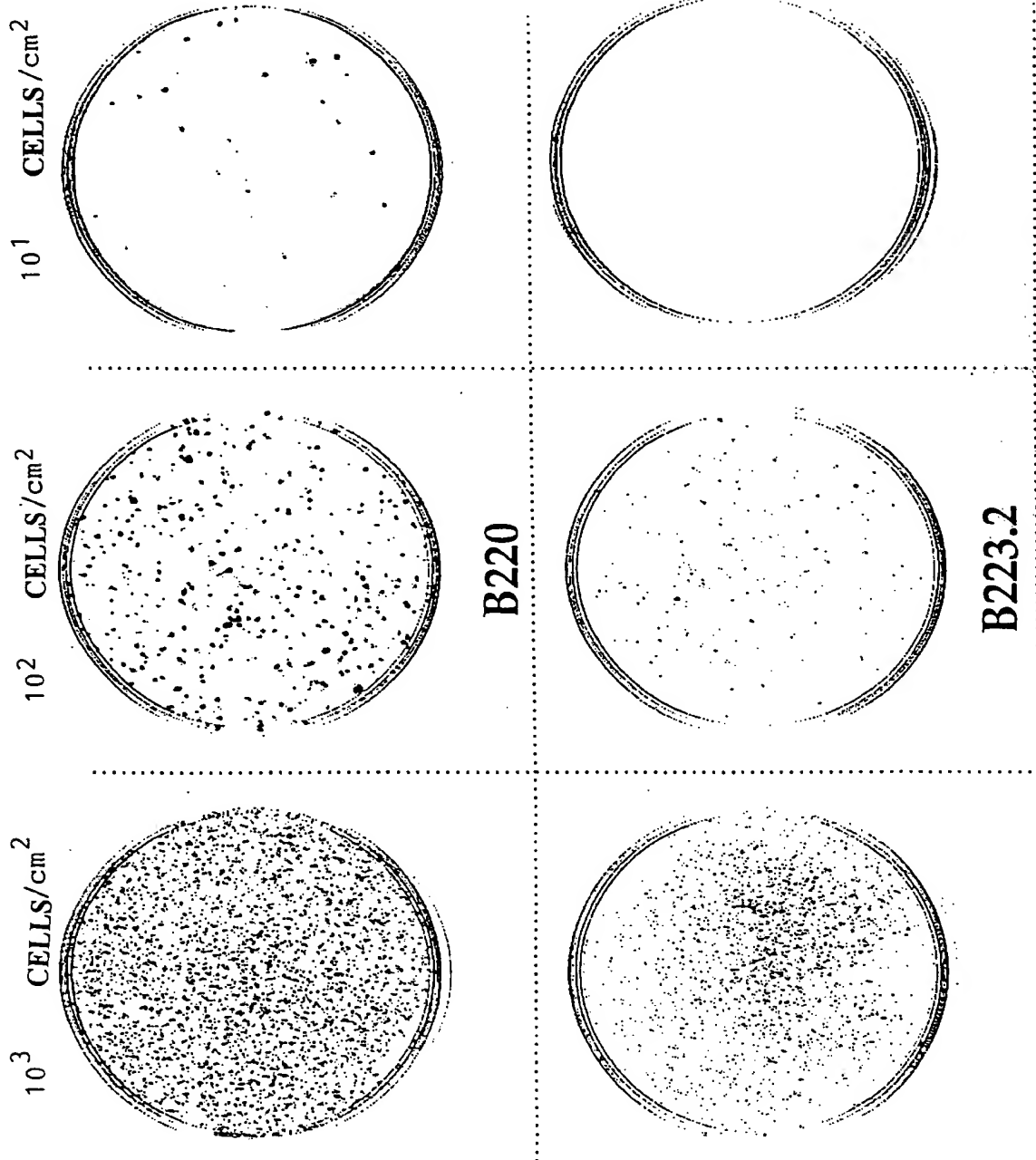


FIG. 16A

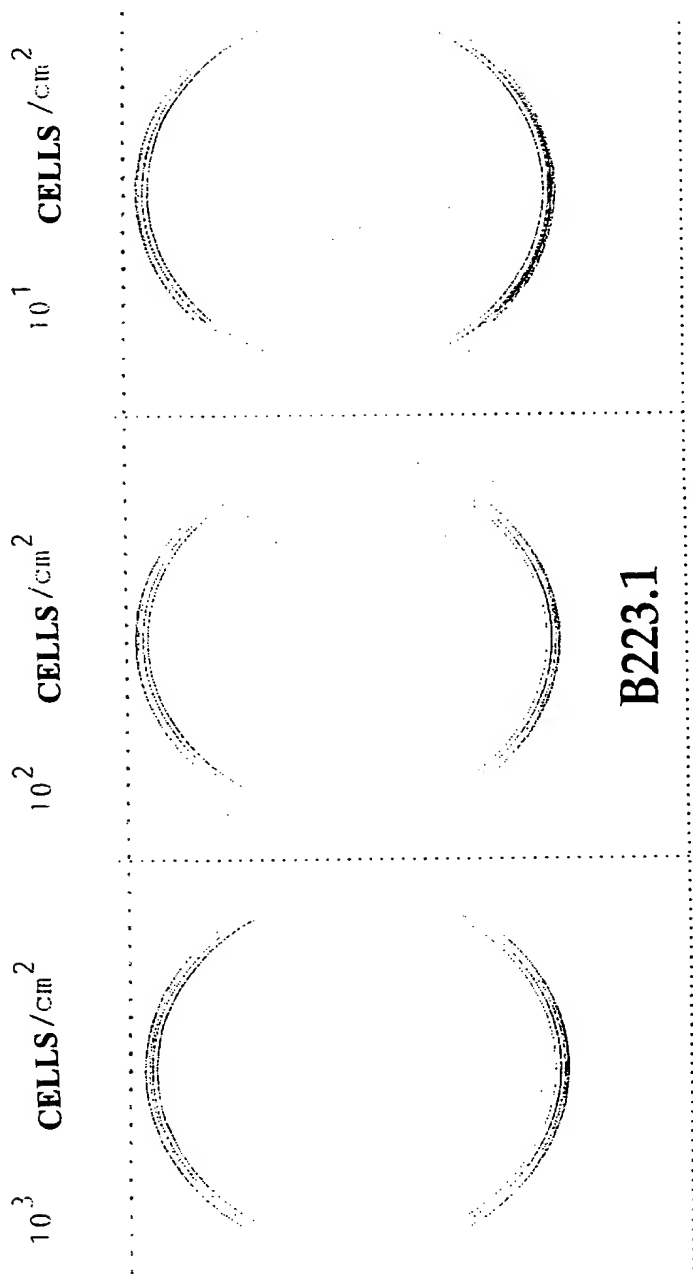


FIG. 16B



FIG. 17A

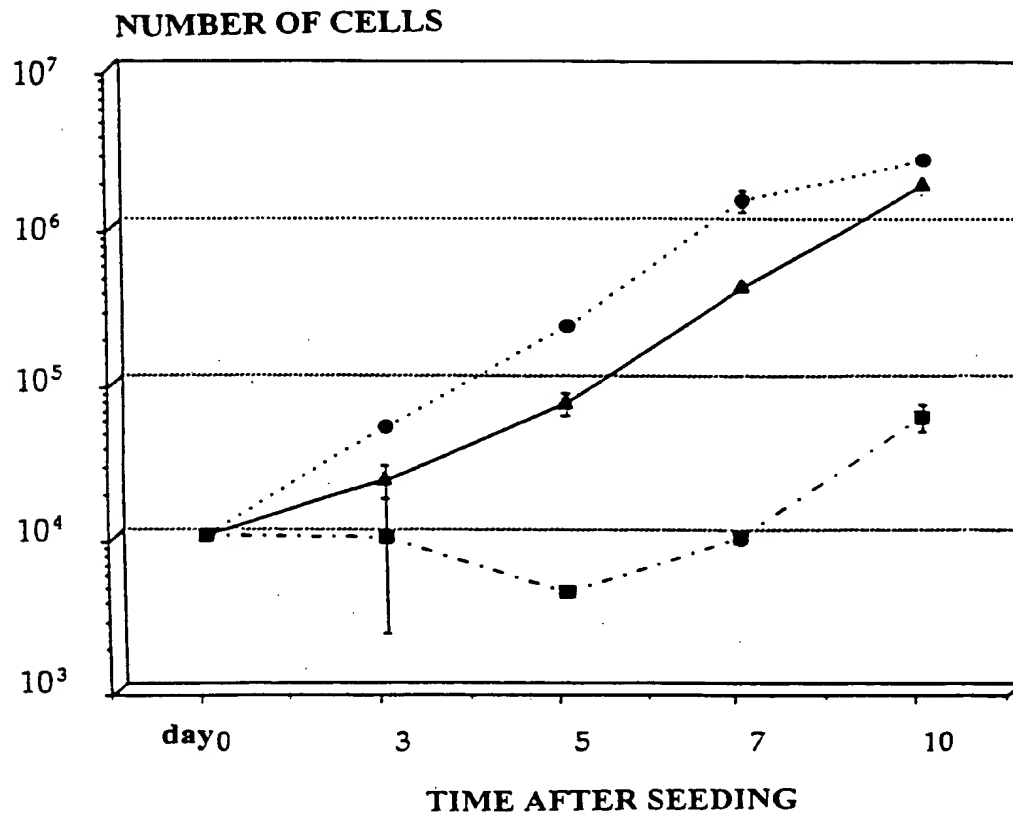
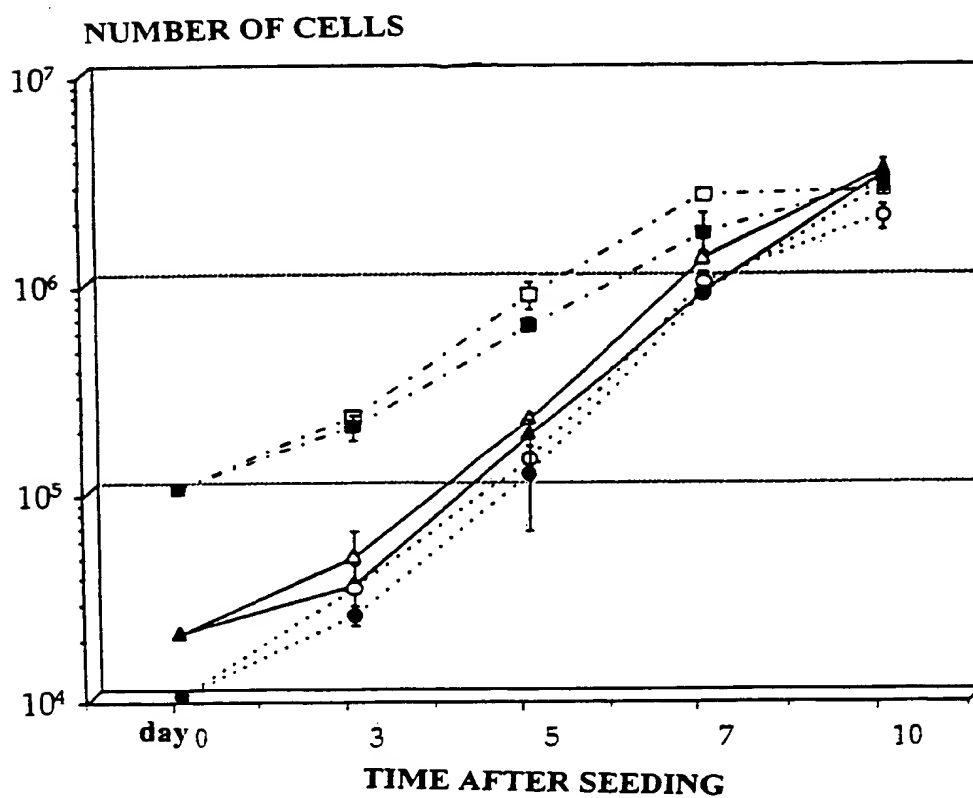
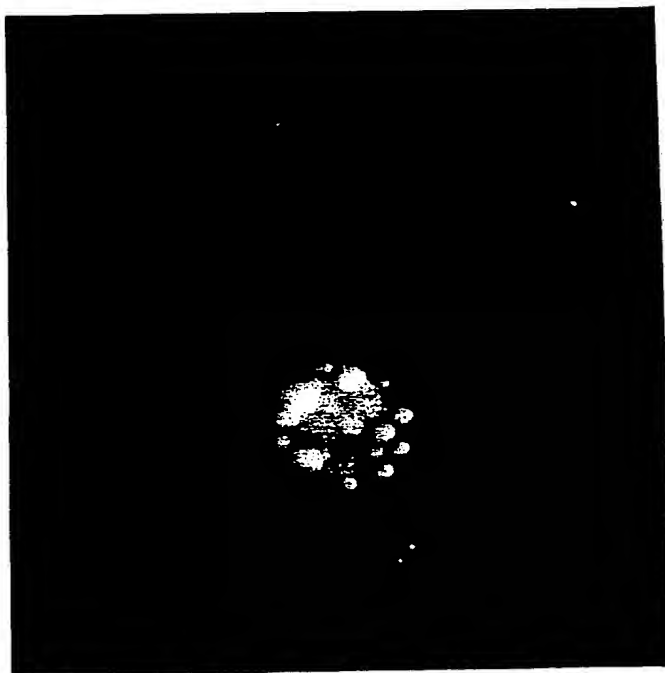


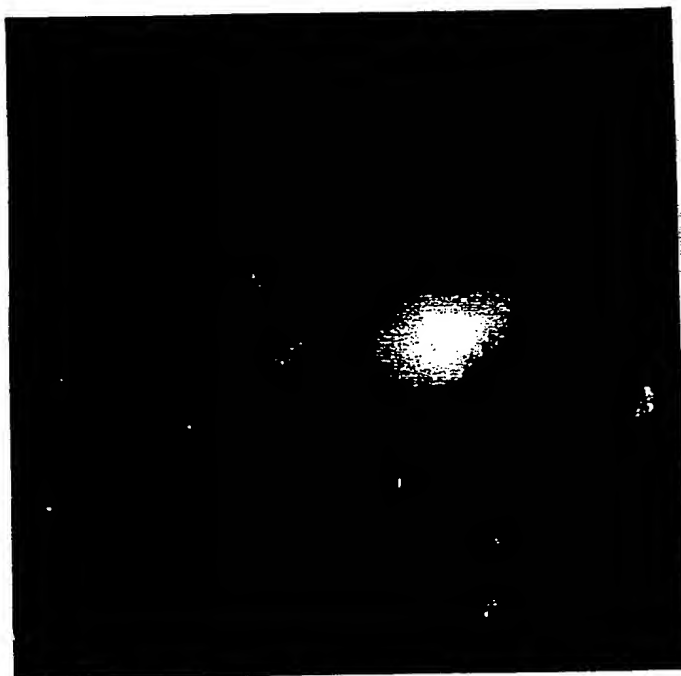
FIG. 17B





GFPkin17NLS-CT

FIG. 18B



GFPkin17 Δ CT

FIG. 18A